

Serial Number: 10/066,127CRF Processing Date: 5/30/2002
Edited by: AV
Verified by: AV (STIC staff) Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____. Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other:



OIPE

RAW SEQUENCE LISTING DATE: 05/30/2002
 PATENT APPLICATION: US/10/066,127 TIME: 07:53:08

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF3\05302002\J066127.raw

3 <110> APPLICANT: HYBRIGENICS
 4 Pierre, LEGRAIN
 6 <120> TITLE OF INVENTION: Identification of the Anti-s28 Factor in Helicobacter
 pylori, in
 7 Campylobacter jejuni and in Pseudomonas aeruginosa and Application Thereof
 9 <130> FILE REFERENCE: B4797A
 11 <140> CURRENT APPLICATION NUMBER: US 10/066,127
 12 <141> CURRENT FILING DATE: 2002-01-31
 14 <150> PRIOR APPLICATION NUMBER: US 60/265,465
 15 <151> PRIOR FILING DATE: 2001-01-31
 17 <160> NUMBER OF SEQ ID NOS: 29
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 90
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Helicobacter pylori
 26 <220> FEATURE:
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 28 <222> LOCATION: (1)..(90)
 29 <223> OTHER INFORMATION: the Selected Interacting Domain (SID(r)) of HP1122
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 35 atggcaaagg atttattggg gataagctag 90
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 29
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Helicobacter pylori
 43 <220> FEATURE:
 W--> 44 <221> NAME/KEY: SID1122
 45 <222> LOCATION: (1)..(29)
 46 <223> OTHER INFORMATION:
 49 <400> SEQUENCE: 2
 51 Ile Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu
 52 1 5 10 15
 55 Thr Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
 56 20 25
 59 <210> SEQ ID NO: 3
 60 <211> LENGTH: 177
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Helicobacter pylori
 64 <220> FEATURE:
 W--> 65 <221> NAME/KEY: SID1032
 66 <222> LOCATION: (1)..(177)
 67 <223> OTHER INFORMATION: the Selected Interacting Domain (SID(r)) HP1032

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70 <400> SEQUENCE: 3
71 aaagcgctga atcaaatgag cgaaagagag caaatcctta tccagctta ttactttgaa 60
73 gagttgaatt tgagcgagat taaagagatt ttaggcatta ctgaatcgcg catttctcaa 120
75 atcattaaag aagtgattaa aaaggtgcgt aaatccttag gagtggatca tggctga 177
78 <210> SEQ ID NO: 4
79 <211> LENGTH: 58
80 <212> TYPE: PRT
81 <213> ORGANISM: Helicobacter pylori
83 <220> FEATURE:
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85 <222> LOCATION: (1)..(58)
86 <223> OTHER INFORMATION:
89 <400> SEQUENCE: 4
91 Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln Ile Leu Ile Gln Leu
92 1 5 10 15
95 Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile Lys Glu Ile Leu Gly
96 20 25 30
99 Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys Glu Val Ile Lys Lys
100 35 40 45
103 Val Arg Lys Ser Leu Gly Val Asp His Gly
104 50 55
107 <210> SEQ ID NO: 5
108 <211> LENGTH: 231
109 <212> TYPE: DNA
110 <213> ORGANISM: Helicobacter pylori
112 <220> FEATURE:
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114 <222> LOCATION: (1)..(231)
115 <223> OTHER INFORMATION: the ORF of sigma28 factor
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119 atgaatatca aattaaagga ttttacaatg attaatgccg tttcttctct tgctccggtg 60
121 cagtcttgg ggaattataa gcgtgtggaa aagaatgaaa aagttgaaaa caatgaggcc 120
123 gctttgata gggtagctga gatcaagaaa gcgattgaaa ataaccagta taaaatcaac 180
125 ttgcattgaga cttctcacaa aatggcaaag gatttattgg ggataagcta g 231
128 <210> SEQ ID NO: 6
129 <211> LENGTH: 76
130 <212> TYPE: PRT
131 <213> ORGANISM: Helicobacter pylori
133 <220> FEATURE:
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135 <222> LOCATION: (1)..(76)
136 <223> OTHER INFORMATION:
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141 Met Asn Ile Lys Leu Lys Asp Phe Thr Met Ile Asn Ala Val Ser Ser
142 1 5 10 15
145 Leu Ala Pro Val Gln Ser Leu Gly Asn Tyr Lys Arg Val Glu Lys Asn
146 20 25 30
149 Glu Lys Val Glu Asn Asn Glu Ala Ala Leu Asp Arg Val Ala Glu Ile
150 35 40 45

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153 Lys Lys Ala Ile Glu Asn Asn Gln Tyr Lys Ile Asn Leu His Glu Thr
 154 50 55 60
 157 Ser His Lys Met Ala Lys Asp Leu Leu Gly Ile Ser
 158 65 70 75
 161 <210> SEQ ID NO: 7
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 163 <212> TYPE: DNA
 164 <213> ORGANISM: Helicobacter pylori
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 168 <222> LOCATION: (1)..(768)
 169 <223> OTHER INFORMATION: The ORF of anti sigma 28 factor
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 175 aaaaatatag aaaagggtttt gaacgcctat gataagcaac aacaccacca tcaagacgat 120
 177 ctcgcatttc agtatttacc agccgtgcgc gccatggcgt ttcgtctaaa agagcgttg 180
 179 cccagctcta ttgattttaa cgatctggtt tctattggca ctgaagaatt gattaaattt 240
 181 gccaggcgtt atgagagcgc gttaaacgtat tcttttggg ggtatgcgaa gactcgtgtc 300
 183 aatggggcga tggtagat tttgcgtct ttagatgtga tttctcgctc tagcagggaa 360
 185 ctcattaaaaa gcattgatat tgaatcacc aaacaccctt atgagcatgg gaaagagcct 420
 187 agcgatgcgtt attagcgcgaa aactttaggc gaaaatattt gaaaatattaa agaagccaaa 480
 189 acggcgttcag atatttatgc gttagtgccaa atagatgaac aattcaatgc gattgagcaa 540
 191 gatgaaatca ctaaaaaaat tgaagcagaa gagttgttag agcatgtcca aaaagcgttg 600
 193 aatcaaatga gcgaaagaga gcaaattcctt atccagctt attactttga agagttgaat 660
 195 ttgagcggaga taaaagagat ttttaggcatt actgaatcgc gcatttctca aatcattaaa 720
 197 gaagtgattt aaaaaggcgtt taaatcctt ggagtggatc atggctga 768
 200 <210> SEQ ID NO: 8
 201 <211> LENGTH: 255
 202 <212> TYPE: PRT
 203 <213> ORGANISM: Helicobacter pylori
 205 <220> FEATURE:
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 207 <222> LOCATION: (1)..(255)
 208 <223> OTHER INFORMATION:
 211 <400> SEQUENCE: 8
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 214 1 5 10 15
 217 Glu Thr Ser Glu Lys Asn Ile Glu Lys Val Leu Asn Ala Tyr Asp Lys
 218 20 25 30
 221 Gln Gln His His Gln Asp Asp Leu Ala Ile Gln Tyr Leu Pro Ala
 222 35 40 45
 225 Val Arg Ala Met Ala Phe Arg Leu Lys Glu Arg Leu Pro Ser Ser Ile
 226 50 55 60
 229 Asp Phe Asn Asp Leu Val Ser Ile Gly Thr Glu Glu Leu Ile Lys Leu
 230 65 70 75 80
 233 Ala Arg Arg Tyr Glu Ser Ala Leu Asn Asp Ser Phe Trp Gly Tyr Ala
 234 85 90 95
 237 Lys Thr Arg Val Asn Gly Ala Met Leu Asp Tyr Leu Arg Ser Leu Asp
 238 100 105 110

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241 Val Ile Ser Arg Ser Ser Arg Lys Leu Ile Lys Ser Ile Asp Ile Glu
242 115 120 125
245 Ile Thr Lys His Leu Asn Glu His Gly Lys Glu Pro Ser Asp Ala Tyr
246 130 135 140
249 Leu Ala Gln Thr Leu Gly Glu Asn Ile Glu Lys Ile Lys Glu Ala Lys
250 145 150 155 160
253 Thr Ala Ser Asp Ile Tyr Ala Leu Val Pro Ile Asp Glu Gln Phe Asn
254 165 170 175
257 Ala Ile Glu Gln Asp Glu Ile Thr Lys Lys Ile Glu Ala Glu Glu Leu
258 180 185 190
261 Leu Glu His Val Gln Lys Ala Leu Asn Gln Met Ser Glu Arg Glu Gln
262 195 200 205
265 Ile Leu Ile Gln Leu Tyr Tyr Phe Glu Glu Leu Asn Leu Ser Glu Ile
266 210 215 220
269 Lys Glu Ile Leu Gly Ile Thr Glu Ser Arg Ile Ser Gln Ile Ile Lys
270 225 230 235 240
273 Glu Val Ile Lys Lys Val Arg Lys Ser Leu Gly Val Asp His Gly
274 245 250 255
277 <210> SEQ ID NO: 9
278 <211> LENGTH: 65
279 <212> TYPE: PRT
280 <213> ORGANISM: Campylobacter jejuni
282 <220> FEATURE:
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284 <222> LOCATION: (1)..(65)
285 <223> OTHER INFORMATION: Cj1464 protein
288 <400> SEQUENCE: 9

290 Met Ile Asn Pro Ile Gln Gln Ser Tyr Val Ala Asn Thr Ala Leu Asn
291 1 5 10 15
294 Thr Asn Arg Ile Asp Lys Glu Thr Lys Thr Asn Asp Thr Gln Lys Thr
295 20 25 30
298 Glu Asn Asp Lys Ala Ser Lys Ile Ala Glu Gln Ile Lys Asn Gly Thr
299 35 40 45
302 Tyr Lys Ile Asp Thr Lys Ala Thr Ala Ala Ile Ala Asp Ser Leu
303 50 55 60

306 Ile

307 65

310 <210> SEQ ID NO: 10

311 <211> LENGTH: 107

312 <212> TYPE: PRT

313 <213> ORGANISM: Pseudomonas aeruginosa

315 <220> FEATURE:

W--> 316 <221> NAME/KEY: PA3351

317 <222> LOCATION: (1)..(107)

318 <223> OTHER INFORMATION: PA3351 protein

321 <400> SEQUENCE: 10

323 Met Val Ile Asp Phe Asn Arg Leu Asn Pro Gly Ser Thr Pro Ala Thr
324 1 5 10 15

327 Thr Gly Arg Thr Gly Ser Thr Ala Ala Gly Arg Pro Asp Ala Thr Gly

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328	20	25	30	
331	Ala Asp Lys Ala Gly Gln Ala Ala	Thr Ser Ala Pro Lys Ser Gly Glu		
332	35	40	45	
335	Ser Val Gln Ile Ser Glu Thr Ala Gln Asn Met Gln Lys Val Thr Asp			
336	50	55	60	
339	Gln Leu Gln Thr Leu Pro Val Val Asp Asn Asp Lys Val Ala Arg Ile			
340	65	70	75	80
343	Lys Gln Ala Ile Ala Asp Gly Thr Tyr Gln Val Asp Ser Glu Arg Val			
344	85	90	95	
347	Ala Ser Lys Leu Leu Asp Phe Glu Ser Gln Arg			
348	100	105		
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352	<211> LENGTH: 32			
353	<212> TYPE: DNA			
354	<213> ORGANISM: Artificial sequence			
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357	<223> OTHER INFORMATION: primer PCR 1550			
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364	<211> LENGTH: 42			
365	<212> TYPE: DNA			
366	<213> ORGANISM: Artificial sequence			
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369	<223> OTHER INFORMATION: primer PCR 1551			
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375	<210> SEQ ID NO: 13			
376	<211> LENGTH: 42			
377	<212> TYPE: DNA			
378	<213> ORGANISM: artificial sequence			
380	<220> FEATURE:			
381	<223> OTHER INFORMATION: linker			
383	<400> SEQUENCE: 13			
384	tgacgcatgc actagtcata tgatgttcct tgtttttga tg		42	
387	<210> SEQ ID NO: 14			
388	<211> LENGTH: 22			
389	<212> TYPE: DNA			
390	<213> ORGANISM: artificial sequence			
392	<220> FEATURE:			
393	<223> OTHER INFORMATION: primer PCR 2386			
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399	<210> SEQ ID NO: 15			
400	<211> LENGTH: 27			
401	<212> TYPE: DNA			
402	<213> ORGANISM: artificial sequence			
404	<220> FEATURE:			
405	<223> OTHER INFORMATION: primer PCR 2387			

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/066,127

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L:65 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
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L:113 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:134 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10